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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=5; day=8; hr=14; min=47; sec=42; ms=77;]

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Reviewer Comments:

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur F?rung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

Missing headings because of the non-ascii character which is shown in the above attachment.

Application No: 10586111

Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-24 16:19:26.908

Finished: 2008-04-24 16:19:28.281

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 373 ms

Total Warnings: 9

Total Errors: 3

No. of SeqIDs Defined: 9

Actual SeqID Count: 9

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)

<210> 1
 <211> 1785
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>
 <221> CDS
 <222> (1)..(1785)

<220>
 <221> N_region
 <222> (1)..(21)
 <223> immunoglobulin kappa chain leader sequence

<400> 1
 atg gag aca gac aca ctc ctg cta tgg gta ctg ctg ctc tgg gtt cca 48
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 ggt tcc act ggt gac tct aga atg gtc cag gcc tcg atg agg agc cca 96
 Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro
 20 25 30
 aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att 144
 Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
 35 40 45
 gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg 192
 Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
 50 55 60
 gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg 240
 Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
 65 70 75 80
 cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg 288
 Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
 85 90 95
 gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg 336
 Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
 100 105 110
 cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta 384
 His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
 115 120 125
 gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tcg tta 432
 Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
 130 135 140
 agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg 480
 Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val

145	150	155	160	
aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa				528
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu				
	165	170	175	
aac atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg				576
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu				
	180	185	190	
att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa				624
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys				
	195	200	205	
aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat				672
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr				
	210	215	220	
gag cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc				720
Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr				
225	230	235	240	
tat atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa				768
Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln				
	245	250	255	
gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa				816
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu				
	260	265	270	
ttc ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt				864
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu				
	275	280	285	
ctt gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga				912
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg				
	290	295	300	
cat ccc tgg atc gga tcc aaa cta gct gag cac gaa ggt gac gcg gcc				960
His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala				
305	310	315	320	
cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act gaa ctg				1008
Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu				
	325	330	335	
gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct ggc tac				1056
Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr				
	340	345	350	
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag				1104
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln				
	355	360	365	
ggg ctg gaa tgg att gga tac att aat cct aac act gct tat act gac				1152
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp				
	370	375	380	

tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac aaa tcc	1200
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser	
385 390 395 400	
tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag gat tct	1248
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser	
405 410 415	
gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt	1296
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe	
420 425 430	
cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc	1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly	
435 440 445	
ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tgc gac att gtg ctg	1392
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu	
450 455 460	
acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg gtc acc	1440
Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr	
465 470 475 480	
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat	1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr	
485 490 495	
caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc	1536
Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser	
500 505 510	
aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga tct gga	1584
Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly	
515 520 525	
aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac ctt gca	1632
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala	
530 535 540	
gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc ggt gct	1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala	
545 550 555 560	
ggc acc aag ctg gaa atc aaa cgg gcg gcc gca ggg ccc gaa caa aaa	1728
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Pro Glu Gln Lys	
565 570 575	
ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat	1776
Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His	
580 585 590	
cat cat tga	1785
His His	
595	

<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro
			20					25					30		
Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile
		35				40						45			
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg
	50					55					60				
Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg
65					70					75					80
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg
				85				90						95	
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu
			100					105					110		
His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu
	115					120					125				
Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu
	130					135					140				
Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val
145					150					155					160
Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu
				165				170						175	
Asn	Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu
			180					185					190		
Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys
	195					200					205				
Asn	Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr
	210				215						220				
Glu	Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr
225					230					235					240
Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln
			245					250						255	
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu
		260						265					270		
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu
	275						280						285		
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg
	290					295					300				
His	Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Gly	Asp	Ala	Ala
305					310					315					320
Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu
			325					330						335	
Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		340						345					350		
Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln
		355					360						365		
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	Thr	Asp
	370					375							380		

Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser
 385 390 395 400
 Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser
 405 410 415
 Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe
 420 425 430
 Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 435 440 445
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
 450 455 460
 Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr
 465 470 475 480
 Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr
 485 490 495
 Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser
 500 505 510
 Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly
 515 520 525
 Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
 530 535 540
 Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala
 545 550 555 560
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Gly Pro Glu Gln Lys
 565 570 575
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 580 585 590
 His His

<210> 3
 <211> 1794
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

<220>
 <221> CDS
 <222> (1)..(1794)

<220>
 <221> N_region
 <222> (1)..(21)
 <223> immunoglobulin kappa chain leader sequence

<400> 3
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 1 5 10 15
 ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg 96
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
 20 25 30

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg	144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met	
35 40 45	
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg	192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp	
50 55 60	
gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat	240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	
65 70 75 80	
cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc	288
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
85 90 95	
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca	384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
115 120 125	
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc	432
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val	
130 135 140	
acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt	480
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
145 150 155 160	
ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg	528
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met	
165 170 175	
tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg	576
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val	
180 185 190	
gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa	624
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
195 200 205	
ctg ctg ata tac ggg gcc tcc aac cgg tac act ggg gtc ccc gat cgc	672
Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	
210 215 220	
ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt	720
Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser	
225 230 235 240	
gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag aat tac agg	768
Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg	
245 250 255	
tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg	816

Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
260 265 270

gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat 864
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
275 280 285

atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga 912
Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
290 29